

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/811,353  
Source: TFW  
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IFWO

## RAW SEQUENCE LISTING

DATE: 02/04/2005

PATENT APPLICATION: US/10/811,353

TIME: 16:22:33

Input Set : A:\sequence.listing.ST25.txt

Output Set: N:\CRF4\02042005\J811353.raw

```

3 <110> APPLICANT: McCray, Paul B.
4     Sanders, David A.
5     Jeffers, Scott A.
6     Davidson, Beverly L.
7     Sinn, Patrick L.
9 <120> TITLE OF INVENTION: PSEUDOTYPED VIRUSES AND METHODS FOR THEIR USE
11 <130> FILE REFERENCE: 290.00670120
13 <140> CURRENT APPLICATION NUMBER: US 10/811,353
14 <141> CURRENT FILING DATE: 2004-03-26
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 681
22 <212> TYPE: PRT
23 <213> ORGANISM: Marburg virus glycoprotein
25 <400> SEQUENCE: 1
27 Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
28 1      5      10      15
31 Lys Asn Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
32      20      25      30
35 Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
36      35      40      45
39 Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
40      50      55      60
43 Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
44 65      70      75      80
47 Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
48      85      90      95
51 Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Asp Pro Pro Thr Asn
52      100     105     110
55 Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
56      115     120     125
59 Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
60      130     135     140
63 Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
64 145     150     155     160
67 Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
68      165     170     175
71 Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
72      180     185     190
75 Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
76      195     200     205
79 Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln

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80      210      215      220
83 Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
84 225      230      235      240
87 Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr
88      245      250      255
91 Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
92      260      265      270
95 Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
96      275      280      285
99 Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
100     290      295      300
103 Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
104 305      310      315      320
107 Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
108      325      330      335
111 Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
112      340      345      350
115 Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
116      355      360      365
119 Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
120     370      375      380
123 Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys
124 385      390      395      400
127 Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser
128      405      410      415
131 Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg
132      420      425      430
135 Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
136      435      440      445
139 Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
140     450      455      460
143 Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
144 465      470      475      480
147 Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
148      485      490      495
151 Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
152      500      505      510
155 Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
156      515      520      525
159 Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
160     530      535      540
163 Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
164 545      550      555      560
167 Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
168      565      570      575
171 Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
172      580      585      590
175 Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
176      595      600      605

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179 Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile
180      610                      615                      620
183 Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
184 625                      630                      635                      640
187 Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
188                      645                      650                      655
191 Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
192                      660                      665                      670
195 Cys Arg Ile Phe Thr Lys Tyr Ile Gly
196      675                      680
199 <210> SEQ ID NO: 2
200 <211> LENGTH: 2046
201 <212> TYPE: DNA
202 <213> ORGANISM: Marburg virus glycoprotein
204 <400> SEQUENCE: 2
205 atgaagacca catgtctctt tatcagtctt atcttaatcc aagggataaa aactctccct      60
207 atttttagaga tagctagtaa caatcaaccc caaaatgtgg attcggtagt ctccggaact      120
209 ctccagaaga cagaagatgt ccattctgat ggattcacac tgagtgggca aaaagttgct      180
211 gattccccct tggaggcatc caagcgatgg gctttcagga caggtgtacc tcccaagaat      240
213 gttgagtata cagaagggga ggaagccaaa acatgctaca atataagtgt aacggatccc      300
215 tctggaaaat ccttgctggt ggatcctcct accaacatcc gtgactatcc taaatgcaaa      360
217 actatccatc atattcaagg tcaaaaccct catgcgcaag ggatcgccct ccatttgtgg      420
219 ggagcatttt tctgtatga tgcattgcc tccacaacaa tgtaccgagg cagagtcttc      480
221 actgaaggga acatagcagc tatgattgtc aataagacag tgcacaaaat gattttctcg      540
223 aggcaaggac aggggtaccg tcacatgaat ctgacttcta ctaataaata ttggacaagt      600
225 aacaatggaa cacaacgaa tgacactgga tgcttcgggt ctcttcaaga atacaactcc      660
227 acgaagaatc aaacatgtgc tccgtccaaa ataccctcac cactgcccac agcccgtcca      720
229 gagatcaaac ccacaagcac cccaactgat gccaccacac tcaacaccac agacccaaac      780
231 aatgatgatg aggacctcat aacatccggt tcagggtccg gagaacagga accctataca      840
233 acttcagatg cggtcactaa gcaagggctt tcatcaacaa tgccaccac tccctcacca      900
235 caaccaagca cgccacagca agaaggaaac aacacagacc attcccaagg tactgtgact      960
237 gaaccaaca aaaccaacac aacggcaca cgcgccatgc cccccacaa caccactgca      1020
239 atctctacta acaacacctc caagaacaac ttcagcacc cctctgtatc actacaaaac      1080
241 accaccaatt acgacacaca gagcacagcc actgaaaatg aacaaaccag tgccccctcg      1140
243 aaaacaaccc tgctccaac aggaaatctt accacagcaa agagcactaa caacacgaaa      1200
245 ggccccacca caacggcacc aaatatgaca aatgggcatt taaccagtcc ctccccacc      1260
247 cccaaccgca ccacacaaca tcttgatat ttcagaaaga aacgaagtat cctctggagg      1320
249 gaaggcgaca tgtttccttt tctggacggg ttaataaatg ctccaattga ttttgatcca      1380
251 gttccaaata caaagacgat ctttgatgaa tcttctagtt ctggtgcttc gggtgaggaa      1440
253 gatcaacatg cctcccccaa tatcagttta actttatcct attttcctaa tataaatgaa      1500
255 aacactgcct actctggaga aaatgagaac gattgtgatg cagagttaag aatttgagc      1560
257 gttcaggagg atgacctggc agcagggtc agttggatac cgttttttgg ccttggaaac      1620
259 gaaggacttt atactgctgg ttttaattaaa aacaaaacaa atttggtctg caggttgagg      1680
261 cgtctagcca atcaaactgc caaatccttg gaactcttat taagagtcac aaccgaggaa      1740
263 aggacatttt ccttaattaa tagacatgcc attgactttc tactcacaag gtggggaggaa      1800
265 acatgcaaag tgcttgacc tgattgttgc attggaatag aagacttgtc caggaatatt      1860
267 tcggaacaaa ttgacaaat caaaaaagat gaacaaaaag aggggactgg ttgggggtcta      1920
269 ggtggtaaat ggtggacatc cgactggggt gttcttacta acttgggcac tttgtacta      1980
271 ttatccatag ctgtcttgat tgctctatcc tgtatttgc gtatctttac caaatatata      2040

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2046

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273 gggtaa
276 <210> SEQ ID NO: 3
277 <211> LENGTH: 676
278 <212> TYPE: PRT
279 <213> ORGANISM: Ebola virus glycoprotein
281 <400> SEQUENCE: 3
283 Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
284 1 5 10 15
287 Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
288 20 25 30
291 Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
292 35 40 45
295 Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
296 50 55 60
299 Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro
300 65 70 75 80
303 Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
304 85 90 95
307 Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
308 100 105 110
311 Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
312 115 120 125
315 Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr
316 130 135 140
319 Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
320 145 150 155 160
323 Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
324 165 170 175
327 Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
328 180 185 190
331 Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
332 195 200 205
335 Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
336 210 215 220
339 Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
340 225 230 235 240
343 Tyr Val Gln Leu Glu Ser Arg Phe Thr Pro Gln Phe Leu Leu Gln Leu
344 245 250 255
347 Asn Glu Thr Arg Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
348 260 265 270
351 Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
352 275 280 285
355 Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
356 290 295 300
359 Glu Leu Ser Phe Thr Ala Val Ser Asn Arg Ala Lys Asn Ile Ser Gly
360 305 310 315 320
363 Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
364 325 330 335
367 Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln

```

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```

368          340          345          350
371 Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
372          355          360          365
375 Ala Thr Ile Ser Thr Ser Leu Arg Pro Pro Ile Thr Lys Pro Gly Pro
376          370          375          380
379 Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu
380 385          390          395          400
383 Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Ala Ser Thr
384          405          410          415
387 Thr Ser Asp Thr Pro Pro Ala Thr Thr Ala Ala Gly Pro Leu Lys Ala
388          420          425          430
391 Glu Asn Thr Asn Thr Ser Lys Gly Thr Asp Leu Leu Asp Pro Ala Thr
392          435          440          445
395 Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
396          450          455          460
399 His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
400 465          470          475          480
403 Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
404          485          490          495
407 Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
408          500          505          510
411 Pro Asn Leu His Tyr Trp Thr Thr Gln Asp Glu Gly Ala Ala Ile Gly
412          515          520          525
415 Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
416          530          535          540
419 Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
420 545          550          555          560
423 Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
424          565          570          575
427 Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
428          580          585          590
431 Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
432          595          600          605
435 Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
436          610          615          620
439 Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
440 625          630          635          640
443 Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
444          645          650          655
447 Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
448          660          665          670
451 Lys Phe Val Phe
452          675
455 <210> SEQ ID NO: 4
456 <211> LENGTH: 2030
457 <212> TYPE: DNA
458 <213> ORGANISM: Ebola virus glycoprotein
460 <400> SEQUENCE: 4
461 atgggtgtta caggaatatt gcagttacct cgtgatcgat tcaagaggac atcattcttt

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60

**VERIFICATION SUMMARY**

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